

SEQUENCE LISTING

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 Itoyama, Kyo
 Hamamura, Tetsuzo

<120> JUVENILE HORMONE ACID METHYLTRANSFERASE
 GENES AND METHODS OF USING SAME

<130> 480230.401USPC

<140> US 10/542,867

<141> 2003-01-20

<150> PCT/JP03/00415

<151> 2003-01-20

<160> 38

<170> PatentIn version 3.1

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gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta 313

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 Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
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 Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
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 Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
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Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp
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 210 215 220
 Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val
 225 230 235 240
 Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser
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 Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg
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 Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
 35 40 45
 gtg ctc atg gac ttt gta aag cca ctg ctc ccg att cgt gga caa ctg 192
 Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
 50 55 60
 gtg ggc aca gac atc tcc agc cag atg gtg cac tat gcc agt aag cat 240
 Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
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 Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
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Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn	
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atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt	432
Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe	
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145 150 155 160	
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Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro	
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Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn	
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Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe	
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gtt tat gaa ggt gta agg act ctg aaa gat aat gta aag gcc att tgt	672
Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys	
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gac ttc ata gac att gtt ata tcc atg aat ttg cag caa ggt gaa aat	768
Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn	
245 250 255	
aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat	816
Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr	
260 265 270	
gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca	864
Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr	
275 280 285	
cat caa aac ttg gtt aag gga ata aat taa tttttatttta caaattaaca	914
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 Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
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 Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
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 Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
 100 105 110
 Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
 115 120 125
 Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
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 145 150 155 160
 Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
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 Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
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 Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
 195 200 205
 Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
 210 215 220
 Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
 225 230 235 240
 Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
 245 250 255

Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
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 agg gat ggc gaa gag gtt gcc ctg tta gac att ggg tgt ggc agc ggg 144
 Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly
 35 40 45

 gac gtg ttg gtg gac tac att cta ccg gtg ctg agc cgc gga agc act 192
 Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr
 50 55 60

 cct gtg gcg cgc gca ttg gcg aca gac atc tcg gag cag atg gtg cgc 240
 Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg
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 cat gca cgt gaa tcg tac cgt cac gtt aag acg atc gag ttc gac acc 288
 His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr
 85 90 95

 ctt gac atc ggc atc aaa ctc gat agt gca aag ttg tcc cgc tgg gga 336
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 100 105 110

 caa ttt agt cac gtt acc tcg ttc tac tgc cta cac tgg gtt cag aat 384
 Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn
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 130 135 140

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 210 215 220

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 225 230 235 240

cag gat agg ttc cta ctg gac tat atc gct gtt gtg cgg cag atg tac 768
 Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr
 245 250 255

ttg acc aaa act ggc agc gaa gag aat gat tgc aat ctt caa ttc ata 816
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Glu	Lys	Tyr	Ile	Ser	Pro	Tyr	Gln	Tyr	Cys	Glu	Asn	Pro	Ala	Ser	Glu
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 Met Asn
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aac gcc gtt ttg tac gaa caa gct aac agc atg cag aag aga gat gca 164
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ctc aac ttt tta gac gac atc tcc cct aaa cta aag tgg aag aag agt 212
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 Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val Thr Ser
 35 40 45 50

atg ctt aaa aag tac atc cct act gac ttc aag ctg ctc ggc tgt gac 308
 Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly Cys Asp
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atc agt gag aag atg gtg aat ttc gcc aat gac cac cat tgc aat gaa 356
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 85 90 95

atg aag gga aaa ttc gac cat gtt ttc tcc ttc tat gcc ttg cac tgg 452
 Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu His Trp
 100 105 110

gtc ttg gat caa gag cgc gta ttc agg aat att tac gat ttg ctg agt 500
 Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu Leu Ser
 115 120 125 130

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 Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro Val Phe
 135 140 145

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 150 155 160

aaa gat gtc gag aaa tac ata tcg cca tac cac gac tca cag gat cca 644
 Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln Asp Pro
 165 170 175

gcg aaa gaa atg aga aaa gta ttg gaa aaa gtt gga tac gtg gac tac 692
 Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val Asp Tyr
 180 185 190

aag gtg gaa tgt aaa aac ttg gtg tat atg tac aac aac ttc gcc agt 740
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 195 200 205 210

tta tgg aaa acc ctt caa gca atc aac cca ttc aac atc ccg aaa gat 788
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 215 220 225

atg gaa gaa gat ttc aaa caa gat tac tta aat att tta aaa gat atg 836
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 230 235 240

aaa att gtg tct aag tat aat acc gat gag gca agt gtg aac ttc aaa 884
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 245 250 255

tat cgg ttg ctt gtc gta cac gct cgc aag ccg gcc tca gaa ttt tag 932
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Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys
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Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro
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Glu Gly Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu
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 His Trp Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu
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 Asp Pro Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val
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 Asp Tyr Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe
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 Ala Ser Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro
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 Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys
 1 5 10 15

aga gat gct atc atg tgt cta gaa gaa tac gct tcg aaa att aag tgg	216
Arg Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp	
20 25 30	
aag aag agt aat aat aat att ctt gac ata ggc tgt ggg gat gga agc	264
Lys Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser	
35 40 45	
gtg act aat atg ctg aag aaa tac atc cct act gag tac aag ttg ctt	312
Val Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu	
50 55 60	
ggc tgt gat att agc gag aag atg gtg aac ttc gcg aat gat cat cat	360
Gly Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His	
65 70 75	
tgt aac gaa cag act tct ttc acc gtg ctc gat att gag gga gac cta	408
Cys Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu	
80 85 90 95	
cct gaa ggt atg aag gga aac ttc gac cac gtt ttc tcg ttc tac gct	456
Pro Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala	
100 105 110	
ctg cac tgg gtt aat aac caa gaa cga gca ttc aaa aac ata tac aac	504
Leu His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn	
115 120 125	
ctt cta agc gag gat ggg gag tgc ttc acg ata ttc gta gcc tgg gct	552
Leu Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala	
130 135 140	
cct gtg ttt gac gtg tac cga gtg ctc gcg cgc aac aac aag tgg agt	600
Pro Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser	
145 150 155	
caa tgg gtg cat gat gtc gac aga tac ata tcg ccc tac cac gac tct	648
Gln Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser	
160 165 170 175	
ttg gag ccg gaa aaa gat tta aag gct atg ata gac aaa att gga ttc	696
Leu Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe	
180 185 190	
gtt gac atc gat gtg gaa tgt aaa gaa ttg gta ttc gtg tac gac aac	744
Val Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn	
195 200 205	
ata cat att ttg cga aaa gcg tta aca gca atc aac cct ttc aaa atc	792
Ile His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile	
210 215 220	
ccc aag gaa aaa tat gat gat ttc atg gaa gac tat atg gat ata ctg	840

Pro Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu
 225 230 235

aaa gaa cta caa att tta gac aag tac aac aat aat tat gaa aag agc 888
 Lys Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser
 240 245 250 255

gtt gaa ttc aat tac cgt ttg ctt gta gtg tat gcc cga aaa cct gac 936
 Val Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp
 260 265 270

tcg cag gat aaa atg tta gaa gct cta aat gga caa acg tag 978
 Ser Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
 275 280

actgaaaaac ttatatTTTT agttacggca aaatacagtg tagaacagtt atttgtagtt 1038

aaggatgaat gtatagtgtat tctcttcagg tttagtttttg ggccctggtat gaaatgtttgt 1098

ttttttaagt aagctatTTT ggtaatgtaa actatTTTTa aaggcaggaa aataatctgt 1158

gtgtgagcaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1193

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 <213> Helicoverpa armigera

<400> 10
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 1 5 10 15

Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp Lys
 20 25 30

Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser Val
 35 40 45

Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu Gly
 50 55 60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys
 65 70 75 80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu Pro
 85 90 95

Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala Leu
 100 105 110

His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn Leu
 115 120 125

Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala Pro
 130 135 140
 Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser Gln
 145 150 155 160
 Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser Leu
 165 170 175
 Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe Val
 180 185 190
 Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn Ile
 195 200 205
 His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile Pro
 210 215 220
 Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu Lys
 225 230 235 240
 Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser Val
 245 250 255
 Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp Ser
 260 265 270
 Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
 275 280

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 <212> DNA
 <213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 11
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17

<210> 12
 <211> 10
 <212> DNA
 <213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 12
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10

<210> 13
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 13
 aagccgcagt aagatggcgg tgttg 25

<210> 14
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 14
 caacaccgcc atcttactgc ggctt 25

<210> 15
 <211> 30
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<220>
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<210> 16
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<210> 17
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 <213> Artificial

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 <213> Artificial

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 <210> 19
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 <212> DNA
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 <220>
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 <223> "n"=A,T,G or C

 <220>
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 <223> "n"=A,T,G or C

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 <210> 20
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 <223> "n"=A,T,G or C

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 <222> (12)..(12)
 <223> "n"=A,T,G or C

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 taraangara anacrtgrtc raa 23

 <210> 21
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
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 <400> 21
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 <210> 22
 <211> 28
 <212> DNA
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 <220>
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 <400> 22
 tatctcctgc gatgtccagc actgtgaa 28

 <210> 23
 <211> 26
 <212> DNA
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 <400> 23
 cgaacagact tctttcaccg tgctcg 26

 <210> 24
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
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 <400> 24

cgagcacggt gaaagaagtc tgttcg 26

<210> 25
 <211> 30
 <212> DNA
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<400> 25
 aaacatatga ataacgccgt tttgtacgaa 30

<210> 26
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 26
 aactcgagct tgcacgaggt tttgtattg 30

<210> 27
 <211> 30
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 <213> Artificial

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<400> 27
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<210> 28
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 <212> DNA
 <213> Artificial

<220>
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<400> 28
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<210> 29
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<213> Artificial

<220>
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<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> "Xaa"=hydrophobic amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> "Xaa"=low molecular weight neutral amino acid

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> "Xaa"=low molecular weight neutral amino acid

<400> 29
Leu Xaa Xaa Gly Xaa Gly Xaa Gly
1          5

<210> 30
<211> 18
<212> PRT
<213> Artificial

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> "Xaa"=any amino acid

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa"=Gln or Glu

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> "Xaa"=His, Lys or Gln

<220>

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<221> MISC_FEATURE
 <222> (13)..(13)
 <223> "Xaa"=hydrophobic amino acid

<400> 30
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 1 5 10 15

Asp Ala

<210> 31
 <211> 9
 <212> PRT
 <213> Artificial

<220>
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<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> "Xaa"=Leu, Val or Ile

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> "Xaa"=Leu, Val or Ile

<400> 31
 Xaa Leu Asp Xaa Gly Cys Gly Asp Gly
 1 5

<210> 32
 <211> 12
 <212> PRT
 <213> Artificial

<220>
 <223> consensus sequence

<220>
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 <223> "Xaa"=Gln, Arg or Lys

<220>
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 <223> "Xaa"=Leu or Val

<220>

<221> MISC_FEATURE
 <222> (10)..(10)
 <223> "Xaa"=Gln or Lys

<400> 32
 Xaa Leu Xaa Gly Cys Asp Ile Ser Glu Xaa Met Val
 1 5 10

<210> 33
 <211> 13
 <212> PRT
 <213> Artificial

<220>
 <223> consensus sequence

<220>
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 <222> (9)..(9)
 <223> "Xaa"=Cys, Thr or Ala

<400> 33
 Phe Asp His Val Phe Ser Phe Tyr Xaa Leu His Trp Val
 1 5 10

<210> 34
 <211> 9
 <212> PRT
 <213> Artificial

<220>
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<220>
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 <222> (2)..(2)
 <223> "Xaa"=Val or Ile

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> "Xaa"=Val, Ile or Leu

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> "Xaa"=Ile or Val

<400> 34
 Pro Xaa Phe Asp Xaa Tyr Arg Xaa Leu
 1 5

<210> 35
 <211> 12
 <212> PRT
 <213> Artificial

<220>
 <223> consensus sequence

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 <223> "Xaa"=Lys or Arg

<400> 35
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 1 5 10

<210> 36
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> consensus sequence

<220>
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 <223> "Xaa"=Ile, Val or Leu

<400> 36
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 1 5 10

<210> 37
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence encoded from DGJF primer

<400> 37
 Met Val Lys Tyr Ala Asn Lys His
 1 5

<210> 38
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence encoded from DGJR primer

<400> 38

Phe Asp His Val Phe Ser Phe Tyr

1

5